IFWO

RAW SEQUENCE LISTING   DATE: 08/05/2004
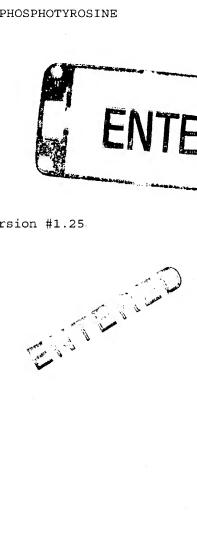PATENT APPLICATION: **US/10/671,589**   TIME: 08:59:10

Input Set : **N:\Crf3\RULE60\10671589.raw**
Output Set: **N:\CRF4\08052004\J671589.raw**

SEQUENCE LISTING

```
 3 (1)  GENERAL INFORMATION:
 5      (i)  APPLICANT: Schlessinger, Joseph
                       Sap, Jan M.
 8     (ii)  TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
 9                               PHOSPHATASE-ALPHA
11    (iii)  NUMBER OF SEQUENCES: 14
13     (iv)  CORRESPONDENCE ADDRESS:
14           (A)  ADDRESSEE: PENNIE & EDMONDS
15           (B)  STREET: 1155 AVENUE OF THE AMERICAS
16           (C)  CITY: NEW YORK
17           (D)  STATE: NEW YORK
18           (E)  COUNTRY: U.S.A.
19           (F)  ZIP: 10036
21      (v)  COMPUTER READABLE FORM:
22           (A)  MEDIUM TYPE: Floppy disk
23           (B)  COMPUTER: IBM PC compatible
24           (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
25           (D)  SOFTWARE: PatentIn Release #1.0, Version #1.25
27     (vi)  CURRENT APPLICATION DATA:
C--> 28      (A)  APPLICATION NUMBER: US/10/671,589
C--> 29      (B)  FILING DATE: 29-Sep-2003
W--> 35      (C)  CLASSIFICATION:
37    (vii)  PRIOR APPLICATION DATA:
33           (A)  APPLICATION NUMBER: US/09/280,597
34           (B)  FILING DATE: 29-MARCH-1999
38           (A)  APPLICATION NUMBER: US 08/015,985
39           (B)  FILING DATE: 10-FEB-1993
41   (viii)  ATTORNEY/AGENT INFORMATION:
42           (A)  NAME: Coruzzi, Laura A.
43           (B)  REGISTRATION NUMBER: 30,742
44           (C)  REFERENCE/DOCKET NUMBER: 7683-020
46     (ix)  TELECOMMUNICATION INFORMATION:
47           (A)  TELEPHONE: (212) 790-9090
48           (B)  TELEFAX: (212) 869-9741/8864
49           (C)  TELEX: 66141 PENNIE
53 (2)  INFORMATION FOR SEQ ID NO: 1:
55      (i)  SEQUENCE CHARACTERISTICS:
56           (A)  LENGTH: 802 amino acids
57           (B)  TYPE: amino acid
58           (D)  TOPOLOGY: linear
60     (ii)  MOLECULE TYPE: protein
62     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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 64 Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
 65  1               5                  10                  15
 67 Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
 68             20                  25                  30
 70 Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
 71         35                  40                  45
 73 Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
 74      50                  55                  60
 76 Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
 77 65                  70                  75                  80
 79 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
 80             85                  90                  95
 82 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
 83             100                 105                 110
 85 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
 86         115                 120                 125
 88 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
 89      130                 135                 140
 91 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
 92 145                 150                 155                 160
 94 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg
 95             165                 170                 175
 97 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
 98         180                 185                 190
100 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
101         195                 200                 205
103 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
104     210                 215                 220
106 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
107 225                 230                 235                 240
109 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
110             245                 250                 255
112 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
113         260                 265                 270
115 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
116     275                 280                 285
118 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
119     290                 295                 300
121 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
122 305                 310                 315                 320
124 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
125             325                 330                 335
127 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
128         340                 345                 350
130 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
131         355                 360                 365
133 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
134     370                 375                 380
136 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile
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137 385                    390                    395                    400
139 Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr
140             405                    410                    415
142 Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro
143             420                    425                    430
145 Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg
146             435                    440                    445
148 Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr
149         450                    455                    460
151 Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln
152 465                    470                    475                    480
154 Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln
155             485                    490                    495
157 Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr
158             500                    505                    510
160 Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr
161         515                    520                    525
163 Ser Asn Asn Gly Leu Glu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys
164     530                    535                    540
166 Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys
167 545                    550                    555                    560
169 Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile
170             565                    570                    575
172 Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser
173             580                    585                    590
175 Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly
176         595                    600                    605
178 Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp
179     610                    615                    620
181 Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln
182 625                    630                    635                    640
184 Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly
185             645                    650                    655
187 Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu Ser Tyr Thr
188         660                    665                    670
190 Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln
191         675                    680                    685
193 Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser
194     690                    695                    700
196 Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln
197 705                    710                    715                    720
199 Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala
200             725                    730                    735
202 Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val
203             740                    745                    750
205 Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg
206         755                    760                    765
208 Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys
209     770                    775                    780
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211 Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
212 785             790             795             800
214 Phe Lys
217 (2)  INFORMATION FOR SEQ ID NO: 2:
219      (i)  SEQUENCE CHARACTERISTICS:
220           (A)  LENGTH: 2409 base pairs
221           (B)  TYPE: nucleic acid
222           (C)  STRANDEDNESS: double
223           (D)  TOPOLOGY: unknown
225     (ii)  MOLECULE TYPE: cDNA
227     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
229 ATGGATTCCT GGTTCATTCT TGTTCTGCTC GGCAGTGGTC TGATATGTGT CAGTGCCAAC      60
231 AATGCTACCA CAGTTGCACC TTCTGTAGGA ATTACAAGAT TAATTAACTC ATCAACGGCA     120
233 GAACCAGTTA AAGAAGAGGC CAAAACTTCA AATCCAACTT CTTCACTAAC TTCTCTTTCT     180
235 GTGGCACCAA CATTCAGCCC AAATATAACT CTGGGACCCA CCTATTTAAC CACTGTCAAT     240
237 TCTTCAGACT CTGACAATGG GACCACAAGA ACAGCAAGCA CCAATTCTAT AGGCATTACA     300
239 ATTTCACCAA ATGGAACGTG GCTTCCAGAT AACCAGTTCA CGGATGCCAG AACAGAACCC     360
241 TGGGAGGGGA ATTCCAGCAC CGCAGCAACC ACTCCAGAAA CTTTCCCTCC TTCAGGTAAT     420
243 TCTGACTCGA AGGACAGAAG AGATGAGACA CCAATTATTG CGGTGATGGT GGCCCTGTCC     480
245 TCTCTGCTAG TGATCGTGTT TATTATCATA GTTTTGTACA TGTTAAGGTT TAAGAAATAC     540
247 AAGCAAGCTG GGAGCCATTC CAATTCTTTC CGCTTATCCA ACGGCCGCAC TGAGGATGTG     600
249 GAGCCCCAGA GTGTGCCACT TCTGGCCAGA TCCCCAAGCA CCAACAGGAA ATACCCACCC     660
251 CTGCCCGTGG ACAAGCTGGA AGAGGAAATT AACCGGAGAA TGGCAGACGA CAATAAGCTC     720
253 TTCAGGGAGG AATTCAACGC TCTCCCTGCA TGTCCTATCC AGGCCACCTG TGAGGCTGCT     780
255 TCCAAGGAGG AAAACAAGGA AAAAAATCGA TATGTAAACA TCTTGCCTTA TGACCACTCT     840
257 AGAGTCCACC TGACACCGGT TGAAGGGGTT CCAGATTCTG ATTACATCAA TGCTTCATTC     900
259 ATCAACGGTT ACCAAGAAAA GAACAAATTC ATTGCTGCAC AAGGACCAAA AGAAGAAACG     960
261 GTGAATGATT TCTGGCGGAT GATCTGGGAA CAAAACACAG CCACCATCGT CATGGTTACC    1020
263 AACCTGAAGG AGAGAAAGGA GTGCAAGTGC GCCCAGTACT GGCCAGACCA AGGCTGCTGG    1080
265 ACCTATGGGA ATATTCGGGT GTCTGTAGAG GATGTGACTG TCCTGGTGGA CTACACAGTA    1140
267 CGGAAGTTCT GCATCCAGCA GGTGGGCGAC ATGACCAACA GAAAGCCACA GCGCCTCATC    1200
269 ACTCAGTTCC ACTTTACCAG CTGGCCAGAC TTTGGGGTGC CTTTTACCCC GATCGGCATG    1260
271 CTCAAGTTCC TCAAGAAGGT GAAGGCCTGT AACCCTCAGT ATGCAGGGGC CATCGTGGTC    1320
273 CACTGCAGTG CAGGTGTAGG GCGTACAGGT ACCTTTGTCG TCATTGATGC CATGCTGGAC    1380
275 ATGATGCATA CAGAACGGAA GGTGGACGTG TATGGCTTTG TGAGCCGGAT CCGGGCACAG    1440
277 CGCTGCCAGA TGGTGCAAAC CGATATGCAG TATGTCTTCA TATACCAAGC CCTTCTGGAG    1500
279 CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA    1560
281 ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA    1620
283 ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG    1680
285 AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGATCAT TCCAGTTAAG    1740
287 CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG    1800
289 GACTCCTATA TCGCCAGCCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG    1860
291 ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG    1920
293 GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG    1980
295 GAACTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCACCAAC    2040
297 ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG    2100
299 GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG    2160
301 CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG    2220
303 ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC    2280
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305 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG    2340
307 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC    2400
309 TTCAAGTAA                                                            2409
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312 (2) INFORMATION FOR SEQ ID NO: 3:
314   (i) SEQUENCE CHARACTERISTICS:
315   (A) LENGTH: 793 amino acids
316   (B) TYPE: amino acid
317   (D) TOPOLOGY: linear
319   (ii) MOLECULE TYPE: protein
321   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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323 Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His
324  1               5                  10                  15
326 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr
327              20                  25                  30
329 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys
330          35                  40                  45
332 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr
333      50                  55                  60
335 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn
336  65                  70                  75                  80
338 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser
339              85                  90                  95
341 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln
342              100                 105                 110
344 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
345          115                 120                 125
347 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
348      130                 135                 140
350 Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
351 145                 150                 155                 160
353 Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
354              165                 170                 175
356 His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
357              180                 185                 190
359 Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
360          195                 200                 205
362 Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg
363      210                 215                 220
365 Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
366 225                 230                 235                 240
368 Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
369              245                 250                 255
371 Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
372          260                 265                 270
374 Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
375          275                 280                 285
377 Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
378      290                 295                 300
380 Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/05/2004
PATENT APPLICATION: US/10/671,589   TIME: 08:59:11

Input Set : N:\Crf3\RULE60\10671589.raw
Output Set: N:\CRF4\08052004\J671589.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos.8,12,21,22,24,25,27,28,30,37,39,47,57,72,77,89,94,95,99,104
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Seq#:9; Xaa Pos.155,170,174,176,179,180,181,182,183,186,205,211,212,214,215
Seq#:9; Xaa Pos.217,222,227,230,232,240,244,247
Seq#:14; Xaa Pos.10,20,21,22,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:14; Xaa Pos.39,40,41,42,43,55,67,70,87,95,96,97,99,100,103,105,106,112
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Seq#:14; Xaa Pos.205,209,212,213,214,218,222,224,228,229,244,247,254,257
Seq#:14; Xaa Pos.264,265,266,267

VERIFICATION SUMMARY   DATE: 08/05/2004
PATENT APPLICATION: **US/10/671,589**   TIME: 08:59:11

          Input Set : **N:\Crf3\RULE60\10671589.raw**
          Output Set: **N:\CRF4\08052004\J671589.raw**

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:1145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14